

FIGURE 1

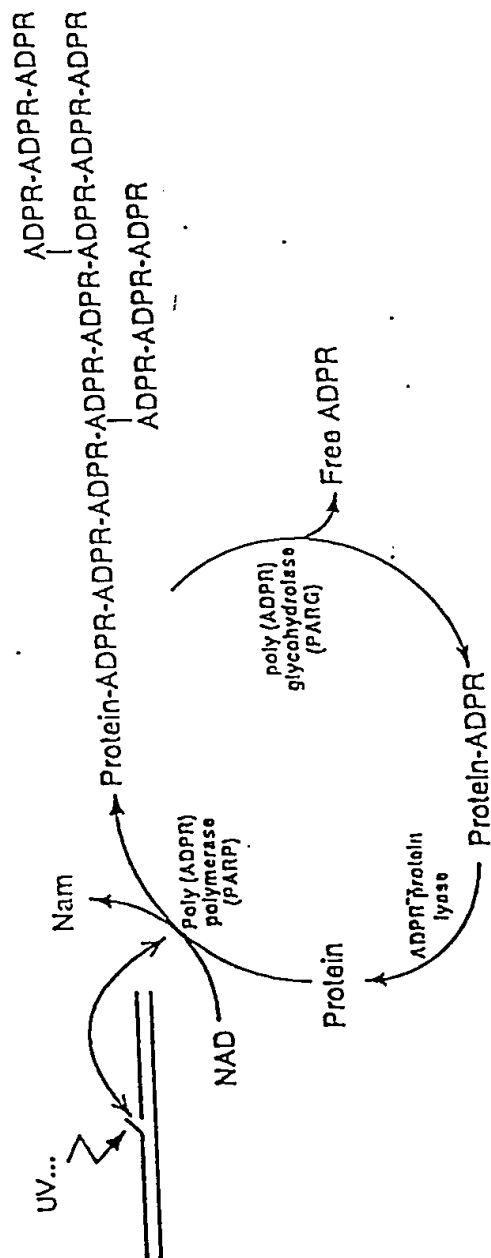
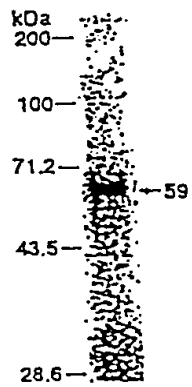


FIGURE 2



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FIGURE 3

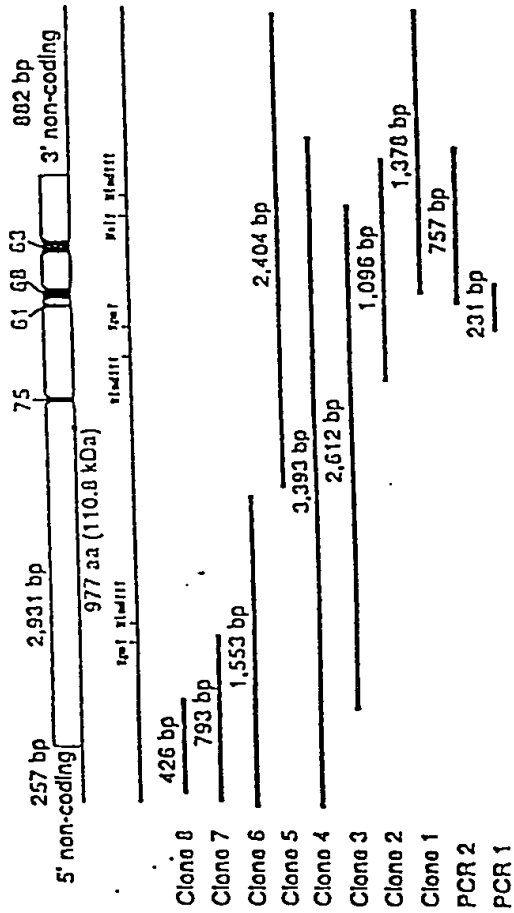


FIGURE 4

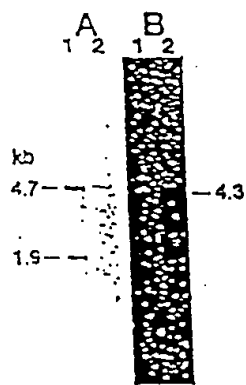


FIGURE 5

bPARG	(422)	ED...	KRKEQCEMKHQ RTE..	RKIPKYIPPH	SEQ ID NO: 19
hPARG	(421)	ED...	RRKEQWETKHQ RTE..	RKIPKYVPPH	SEQ ID NO: 20
mPARG	(413)	ED...	RRKEQCEVRHQ RTE..	RKIPKYIPPN	SEQ ID NO: 21
CePARG	(29)	HQVPTMKRRKL	TEHGNTTESLLKEDPEEPKS		SEQ ID NO: 22
hPARG	(205)	EG...	KRKGD..	VDEVAKKSKKEKDK	SEQ ID NO: 23
mPARG	(205)	EG...	KRKGD..	TDEVAKKSKRKETDK	SEQ ID NO: 24
bPARG	(208)	EG...	KRKGD..	IDVTKKKSKKEKDK	SEQ ID NO: 25
aPARG	(205)	EG...	KRKGE..	NVVAKKSKRKEKEK	SEQ ID NO: 26
XIPARP	(204)	EG...	KRKAD..	HSAA TKKKIKKEKEK	SEQ ID NO: 27
DmPARG	(202)	EELPDTKRAKM.	ELSDTNEEGEKKQR.....		SEQ ID NO: 28
SpPARG	(205)	EGVSSAKKAKI.	EKIDEEDAAS TKELTEKIKK		SEQ ID NO: 29

FIGURE 6

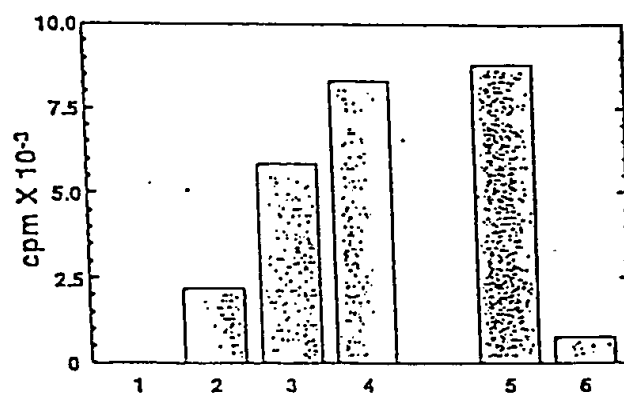


FIGURE 7

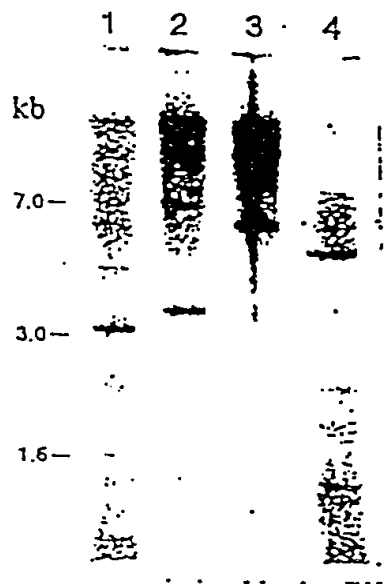


FIGURE 8

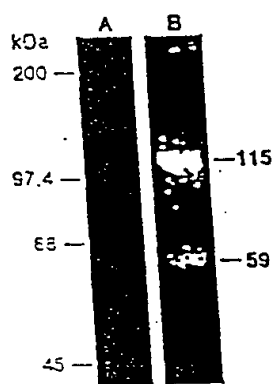


FIGURE 9

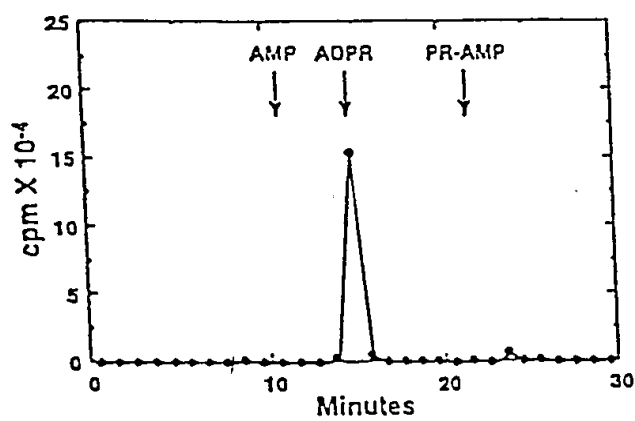


FIGURE 10

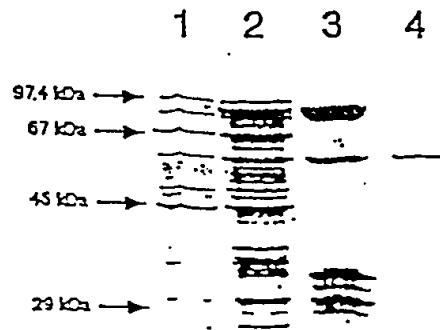


FIGURE 12

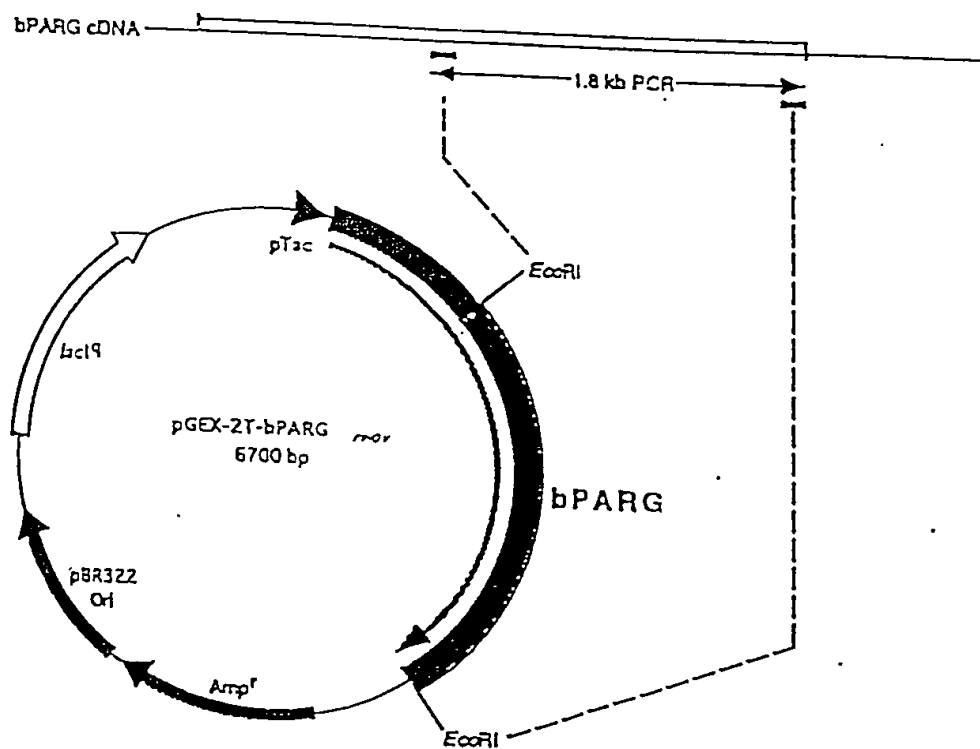


FIGURE 13

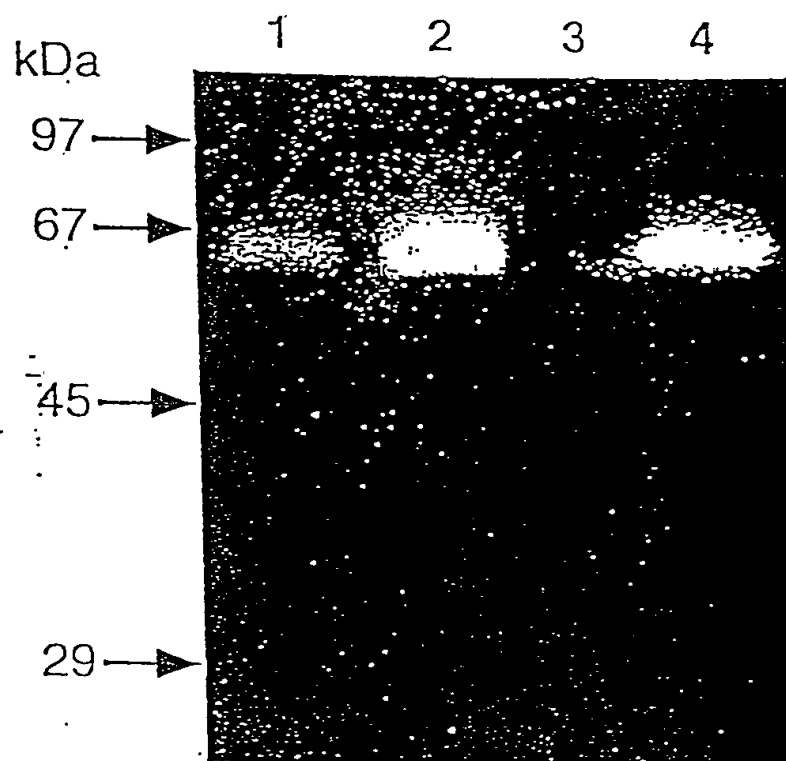
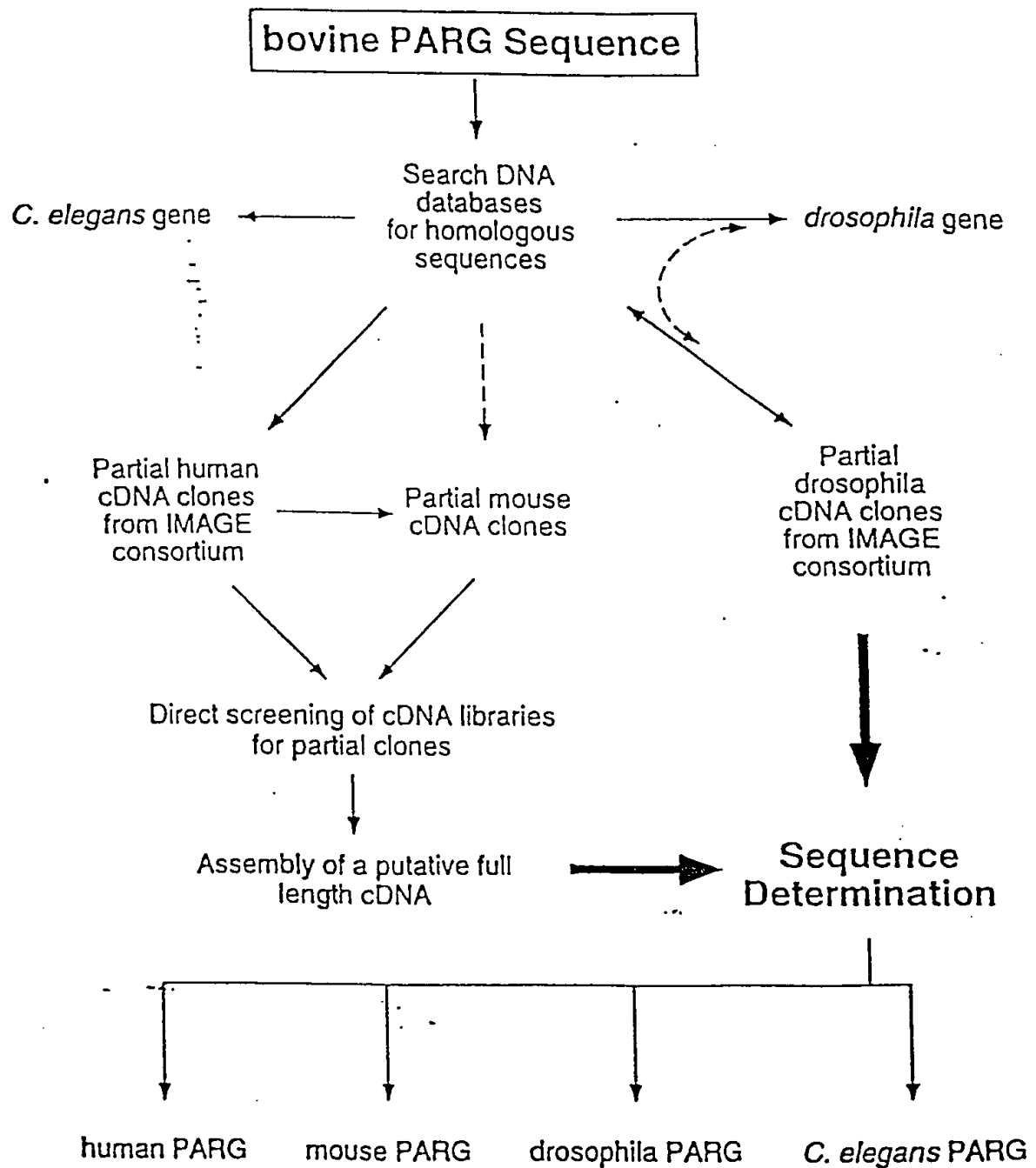


FIGURE 14

Strategy to Obtain Homologous PARG Sequences



Domain Organization of PARs

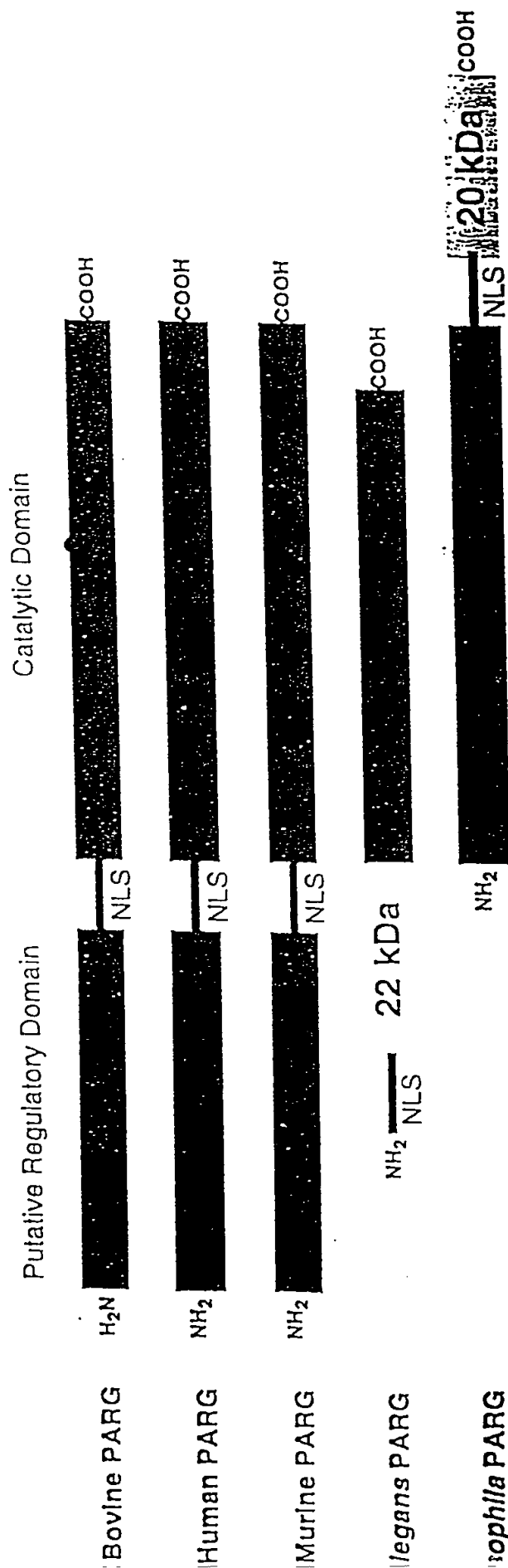


FIGURE 16

Multiple Alignment of Amino Acid Sequences of PARG from Different Species

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Bparg 1 MSAGPGCEPCTKRPRMDAAATSPPAASDARSFPGRQRRVLDSPKDAFVQFRVPPSSSGCALGRAGQRRGSATSLVFKQKXITSMNDIEGIXTVESESLSK
Hparg 1 MNAGPGCEPCTKATRWGAATIS.PAASDARSFPGRQRRVLDSPKDAFVQFRVPPSSSPACVPGQAGQRRGSATSLVFKQKXITSMNDITKGIKTANESLDSK
Mparg 1 MSAGPGWEPCTKA.RWGAAGTSAPTASDSRFPGRQRRVLDSPKDAFVQFRVPPSSSPACVSGRAGPHERGNATSPVFKQKXITITMNDITKPKTARSE...SK
Dparg 1 -----
Ceparg 1 -----

Bparg 101 EHNNTREESHMSSVQKDNFIQHNMKLEWVSQLGFDKSPVEKGTQYLKQHQTAAAMCKWQNEGPHSERLLESEPPAVTLVPEQPSHANVDQSSPKDDSDT
Hparg 100 EHNNTREESHMSSVQKDNFIQHNMKLEWVSQLSLDKSLTEKSTQILNQHQTAAMCKWQNEGCKHTRQLLESEPPQTVTLVPEQPSHANIDRSPQDDSDT
Mparg 97 EHNNTREIDSMSVQKDNFIQHKVLEWVQLNLDKSPTEKSSQILNQHQTAASVCKWQNEGCKHTRQLLESEPPAGTPLPKQLSHANIGQSPHTDDSDT
Dparg 1 -----
Ceparg 1 -----MSKKFLELGDPTVQDEKIDEDY

Bparg 201 NSESRDNHQOPLTEVKL...ANAKQTMEDRQGRKARSHQKCKKACHPAEACAGCQOQEDDVVSESPLESDTGSESDVGTGLKNANRLMRQESSLGMSPPFEK
Hparg 200 DSEHRDMQOPLTTIVKL...ANAKQTMEDRQGRKARSHQKCKKACHPAEACAGCQOQEDDVVSESPLESDTGSESDVGTGLKNANRLMRQESSLGMSPPFEK
Mparg 197 DSEHRDMHQOPLTPIKL...ANTKPTVGDGQ...ARSECKCKSGSRQSVEDCTGCGQOQEDDVVSESPLESDTGSESDVGTGLKNANRLMRQESSLGMSPPFEK
Dparg 1 -----
Ceparg 23 VGVGFARQVPTMKRRKLTREHNTTESKEDPERPKSRDVFVSSQSSDESQEDSAENPRIAEVSENCENLTETLKISNIESLDNVTERRSEETLDN...HK

Bparg 298 ESEPESPMDVDMSKNSCQDSADDEETSPGFDE.QEDSSSAQTANKPSRFQPRREADTELKRRSSAKGGEIRLHPQFEGGESRAGMN.DVFAKRPGSTSLM
Hparg 297 ESEPESPMDVDMSKNSCQDSADDEETSPGFDE.QEDSSSAQTANKPSRFQPRREADTELKRRSSAKGGEIRLHPQFEGGESRAGMN.DVFAKRPGSTSLM
Mparg 291 ESEPESPMDVDMSKNSCQDSADDEETSPGFDE.QEDSSSAQTANKPSRFQPRREADTELKRRSSAKGGEIRLHPQFEGGESRAGMN.DVFAKRPGSTSLM
Dparg 1 -----
Ceparg 119 STEPHEE.DVNMKSHIDVAINSDEDELVLLENHKKSHRDGEQVQQLS...QDLFADDQELIEYPGIMKDTTTLQDITDSEVETAKQHEETADSTFVG

Bparg 396 VECRNSKQHGKRDSDKITDEFMRVPAEDRRKEQCEMKHQRTERRKIPKXIIPPELSPDKKWLGTPIEM...RRMPRCGIRLPLRPSANHTVTIRVDLLRIG
Hparg 395 VECRNSKQHGKRDSDKITDEFMRVPAEDRRKEQCEMKHQRTERRKIPKXIIPPELSPDKKWLGTPIEM...RRMPRCGIRLPLRPSANHTVTIRVDLLRIG
Mparg 387 VECRNSKQHGKRDSDKITDEFMRVPAEDRRKEQCEMKHQRTERRKIPKXIIPPELSPDKKWLGTPIEM...RRMPRCGIRLPLRPSANHTVTIRVDLLRIG
Dparg 32 ...THRLQK...ALCLNCARMSKSPDGGISIE...TEEE.PENLANSL...DSDWGVSMHAIHRNRQPFELNLPFVTAGLBRVMQLPIRET.
Ceparg 216 EDSKATXTVRTSSSSP...LSTVETCRAPAKGRARMHQLEKRVIAVTEGHLT...LQPDNLKVDPPDRMIRY.CTIPNFPASQ...KLRED.WRYG

Bparg 494 EVPK.PPPTHEKDLMDNKEVKNPCSEQNLIPVEDENGE.RTAGSRMELIQTALLNRLTRPQNLKDAILKINVAISSKKWDFTALIDFMDKVLREAAQHL
Hparg 493 EVPK.PPPTHEKDLMDNKEVKNPCSEQNLIPVEDENGE.RTAGSRMELIQTALLNRLTRPQNLKDAILKINVAISSKKWDFTALIDFMDKVLREAAQHL
Mparg 485 EVPK.PPPTHEKDLMDNKEVKNPCSEQNLIPVEDENGE.RTAGSRMELIQTALLNRLTRPQNLKDAILKINVAISSKKWDFTALIDFMDKVLREAAQHL
Dparg 115 ...PPR.PTKSPCK...WDSEVLPKAPESKYPRENPDGS.TTIDFRWEMIERALLQPIKTCEELQAAIISYNTTIRQWEPFALHQLLDEELDESETRVFP
Ceparg 303 ...PKIVLPQWRRE.PDSRGR...RDSIFPKRLDGLKCIKTYGFMVGLLE...HMWE...FDPDITEK...LPAL.EHTYKMSSELVGRREV

Bparg 592 QSILPDMVKIALCLPMICTQPIPLLKQKMHESITNSQEQIASLLANAFCTFPRRNA.KMKSEISSYPDINFNRLPFGRRSSRKPPEKLTLCYFRRV...T
Hparg 591 QSILPDMVKIALCLPMICTQPIPLLKQKMHESITNSQEQIASLLANAFCTFPRRNA.KMKSEISSYPDINFNRLPFGRRSSRKPPEKLTLCYFRRV...T
Mparg 583 QSILPDMVKIALCLPMICTQPIPLLKQKMHESITNSQEQIASLLANAFCTFPRRNA.KMKSEISSYPDINFNRLPFGRRSSRKPPEKLTLCYFRRV...T
Dparg 210 EDLLPRIIRLALRLPDLIQSPVPLLKHHKHWASLSLSQQQISCLLANAFCTFPRRNA.KMKSEISSYPDINFNRLPFGRRSSRKPPEKLTLCYFRRV...T
Ceparg 364 LEKPARVARIKTAEDILPERITRLVGDVE.SATLSKKQCAALVARMFFA...RPDSPPS...FCRILSSDKSICVEXKLKFLPTTF...

Bparg 689 EKK...PIGLVTFTRQS.L.ED.F.PEWERCCKLL...TRLEVTIEGTIEGNGQGMQLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRFLTEVLDE
Hparg 688 EKK...PIGLVTFTRQS.L.ED.F.PEWERCCKPL...TRLEVTIEGTIEGNGQGMQLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRFLTEVLDE
Mparg 680 EKK...PIGLVTFTRQS.L.ED.F.PEWERCCKPL...TRLEVTIEGTIEGNGQGMQLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRFLTEVLDE
Dparg 310 ERDASHVPTGVVTFVRRSLPEH.L.IDNSQSAAPLGDVPLHVDAGETIEDECIGLLQVDFANKILGGGVLCGNGCVQEEIRFVICPELLVCKLFTXCLRP
Ceparg 463 DKMSMDPPDCAVSF.RLTXXDKDFTNEZW.KDKKLSLPEVEFFDMLIEDTAL.CTQVDFANRHLGGCVLNEGVSQEEIRFLMKCPENMVGHLLCEKMKQ

Bparg 779 NECLITGTETQISEYTGIAETIRMA...RSHEDRSE.RDDMQRRTEIIVDAIDALEFR.RYLD...QFVPEKIRRELHKAICGFLRPGVSSNLSAVA
Hparg 778 NECLITGTETQISEYTGIAETIRMS...RSHEDGSE.RDDCRRCTEIVDAIDALEFR.RYLD...QFVPEKIRRELHKAICGFLRPGVSSNLSAVA
Mparg 770 NECLITGTETQISEYTGIAETIRMA...RSHEDGSE.RDDMQRRCTEIVDAIDALEFR.RYLD...QFVPEKIRRELHKAICGFLRPGVSSNLSAVA
Dparg 408 FHALVMLGAERYSTGTGIAETIRMA...GNFEDSTP.RDSSGRQTAIVDAIDALEFA.QSHE...QIREDLMERELHKAICGFLRPGVSSNLSAVA
Ceparg 560 LEAISIVGAIVFSSITGIGETLKNALQPNHESQNTNFRDRFGRLRVETIATDAITLFGKSLDCQTEQLNKANIRKMKKASIGFMSQGPFTNIP.IV

Bparg 668 TGMWGGGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELNRDIYSMTFLTERKLTVGE.VIKLLRLYINEECRNCSTPGP...DICKLIPPIIHA
Hparg 667 TGMWGGGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELNRDIYSMTFLTERKLTVGE.VIKLLRLYINEECRNCSTPGP...DICKLIPPIIHA
Mparg 659 TGMWGGGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELNRDIYSMTFLTERKLTVGE.VIKLLRLYINEECRNCSTPGP...DICKLIPPIIHA
Dparg 495 TGMWGGGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELNRDIYSMTFLTERKLTVGE.VIKLLRLYINEECRNCSTPGP...DICKLIPPIIHA
Ceparg 659 TGMWGGGAFYNGDKPLKPIIQVIAAGVADRPLHFCBFGPELAACKKIIERMKQKDVTLGKSCFSIFS-----

Bparg 961 VESCTQITNQPOQRIGA-----
Hparg 960 VESCAETADHSGQRTGT-----
Mparg 952 VESSAETIDMPCQKAGT-----
Dparg 590 KBELKKVRDVPCEGASAEAGSSRVAGLGGRKSETSAKSSPELNKQPARPQITITQSTDLPAQLSQDNHSSSEDQALLHLSDDDEANAMHEAASLEAKS
Ceparg 727 -----

Bparg 978 -----
Hparg 977 -----
Mparg 969 -----
Dparg 690 SVEISWSSTTSKTSSTATKSMGSGGRQLSLLEMLDTHIEKGSASKRPRKSPMCKSAEGSAKSRKEIDVTDKDEKDDIVD
Ceparg 727 -----

```


FIGURE 17

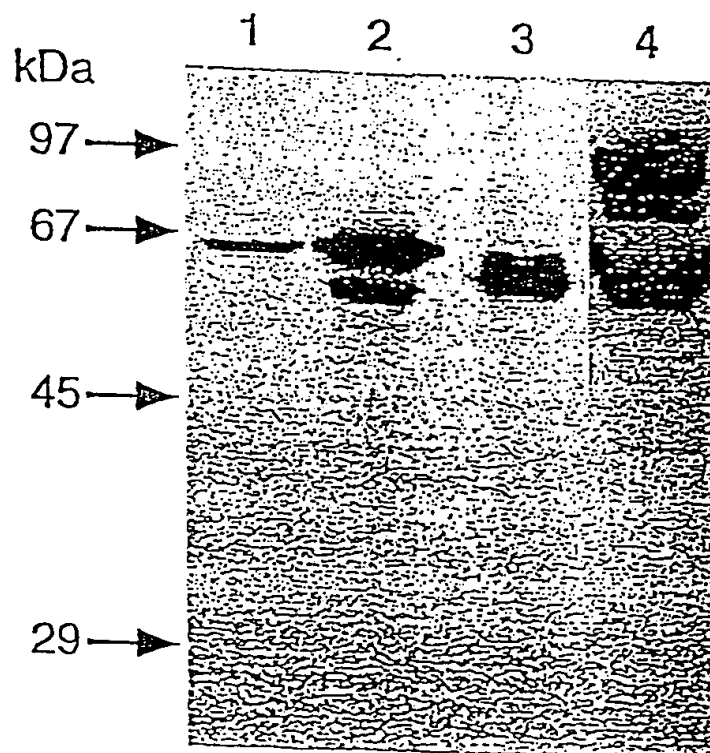
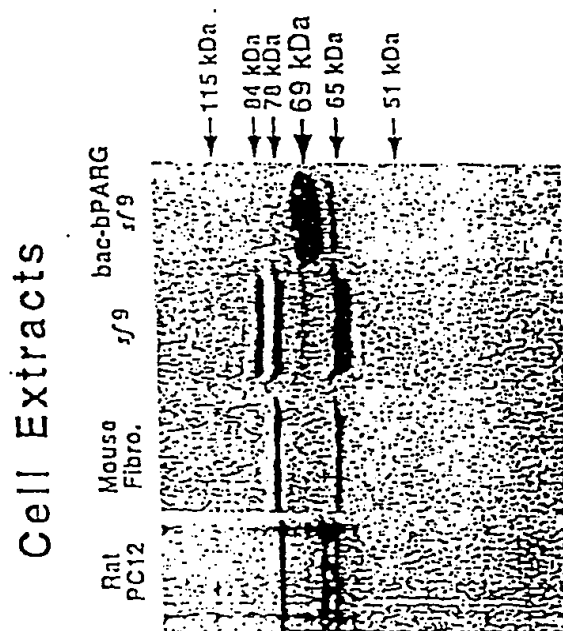


FIGURE 18

B



A

Bovine Tissue

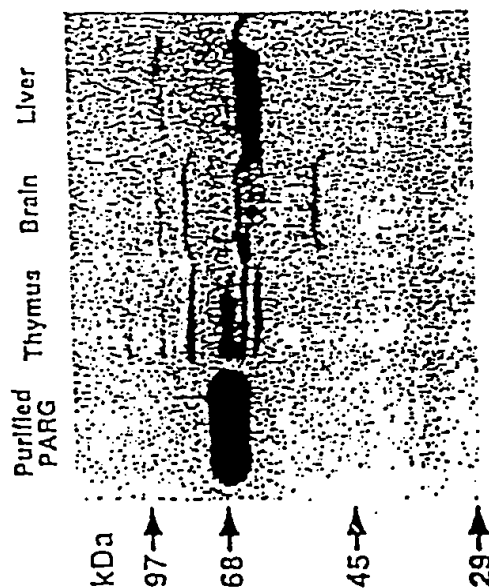
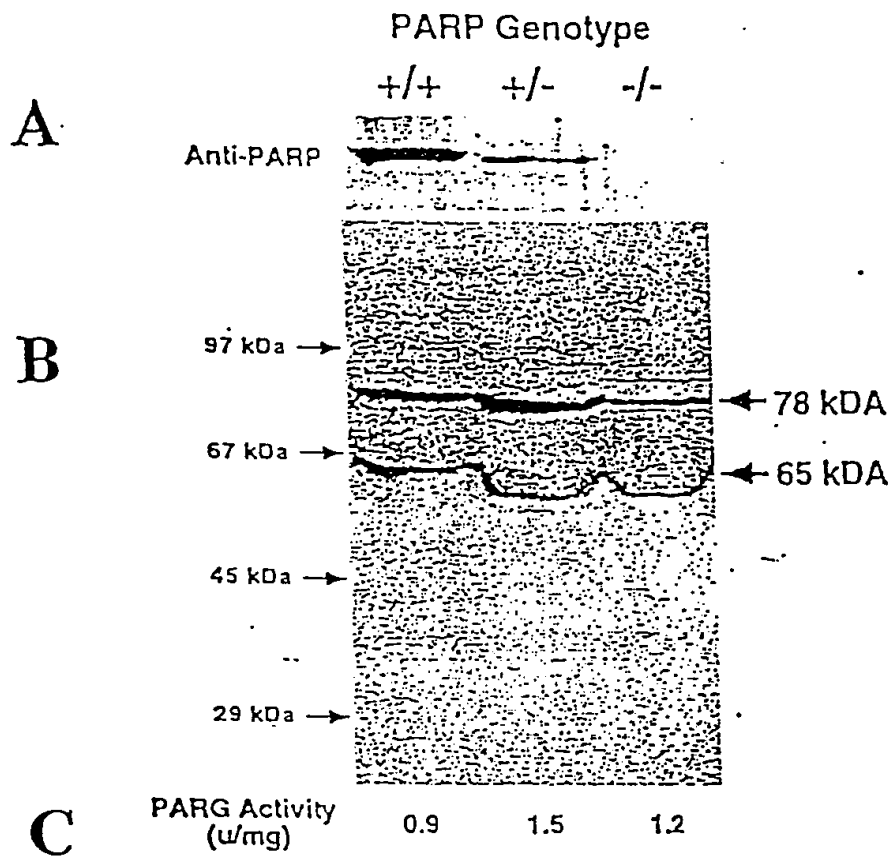


FIGURE 19



Genomic cloning of the PARG gene

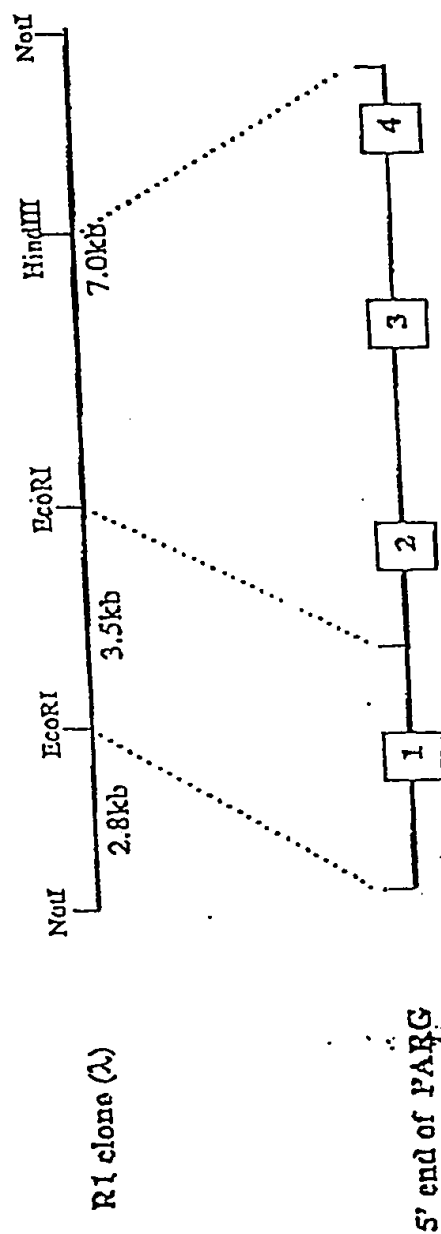


FIGURE 20

FIGURE 21-4-55

